REMARKS

Claims 1-52 and 54 will remain pending following the entry of the foregoing amendments.

Claims 7-17, 23, 24, 44, 45, 47-51 and 54 were identified by the Examiner in the Office Action of January 4, 2006, as being within invention Group II, which was provisionally elected, with traverse, by Applicants in the timely-filed Response to Restriction Requirements filed February 14, 2006. In the present Office Action, the Examiner withdrew from consideration claims not only the claims of the non-elected invention Groups I and III-XX, but also claims 9-12, 44, 45, 47-51 and 54 from Group II, without explanation. Reconsideration, reinstatement and examination of at least these claims from elected Group II are respectfully solicited.

Of the claims presently remaining under consideration by the Examiner, namely claims 7, 8, 13-17, 23 and 24, only claim 7 is an independent claim. All of these claims have been amended to more particularly point out and distinctly claim the subject matter which Applicants regard as the invention set forth in such claims. Claims 8, 13, 14, 17, 23 and 24 have been amended to refer to and depend from "claim 7," rather than "Claim 7." Claims 7 and 8 have been amended to use the more traditional abbreviation "SEQ ID NO:," rather than "SEQ ID No:" when referring to specific sequences. These merely relate to minor syntactical or typographical aspects and clearly are not new matter. Claim 8 has been amended to delete a portion of original claim 8, and that clearly adds no new matter. Claim 7 has been amended to delete portions of original claim 7, and that, too clearly adds no new matter. In part (b) of claim 7, language has been added that is supported at least by the locations of the application as filed as set forth in the comments below regarding the rejections under 35 U.S.C. §§ 101 and 112. Since no new matter has been added, entry of the foregoing amendments is respectfully requested.

Claim Objections

Host cell

In amended claim 16, the host cell is identified as being "isolated," as suggested by the Examiner in section 3 of the Office Action.

Non-elected subject matter in the claims under consideration

Applicants have retained SEQ ID NOs: 2, 25, 26, 27 and 28 in the claims, at least at this time, since Applicants respectfully submit that these sequences are merely a reasonable number of species of the claimed genus. Consideration of these sequences is respectfully requested.

Priority

There is no need to file English translations of the priority Japanese applications at this time, since Applicants currently do not rely on the priority applications to overcome the prior art Published International Application Publication No. WO 2001/75067 of Drmanac *et al.*(hereinafter "Drmanac").

Claim Rejections – 35 U.S.C. § 101

The specification as filed discloses that a protein encoded by a polynucleotide recited in amended claim 7, specifically, a protein encoded by a polynucleotide comprising the nucleotide sequence encoding the amino acid sequence of SEQ ID NO:1, has the following specific, substantial and credible utilities or well-established utilities: (A) an ability to mediate a signal transduction from a dopamine D1 receptor to an adenylate cyclase, such as in Example 24; (B) an ability to mediate a signal transduction from an adenosine A2a receptor to an adenylate cyclase, such as in Example 25; and (C) as useful for screening of an agonist or antagonist of dopamine D1 receptor or adenosine A2a receptor, such as in Examples 17, 18, 21 and 22. Moreover, among test substances used in the Examples, for example, butaclamol, chlorpromazine, fluphenazine and haloperidol A are known as compounds useful as an active ingredient of an anti-psychotic agent, and apomorphine is known as a compound useful as an active ingredient of an anti-parkinsonian agent. As shown in the Examples, such screening may provide substances useful as active ingredients of therapeutic agents to treat these conditions.

Thus, the specification offers specific evidence and examples to place significance on the particular function and use of the claimed polynucleotides. Reconsideration and withdrawal of the rejections based on 35 U.S.C. § 101 for lack of utility, are respectfully requested.

Claim Rejections – 35 U.S.C. § 112, first paragraph

The polynucleotide claimed in amended claim 7 is supported by either a specific and substantial, credible asserted utility, or by a well-established utility, as mentioned above.

Amended claim 7 recites structural features common to the genus, such as "retains amino acid sequences represented by the amino acid Nos. 119 to 133, 287 to 292, 353 to 359 and 428 to 435 in the amino acid sequence of SEQ ID NO:1", where this recitation is supported by the specification as filed, such as from page 27, line 19, to page 28, line 13. The amino acid sequences represented by the amino acid Nos.126 to 133, 287 to 292, 353 to 359, and 428 to 435 of SEQ ID NO:1 have high homology with the sequences of the GTP binding site and the

GTPase activation site conserved among G protein α subunits, and are identical to the sequences of the GTP binding site and the GTPase activation site of the Gs and Golf proteins belonging especially to the Gs family among the G protein α subunits. The amino acid sequence represented by the amino acid Nos.119 to 126 of SEQ ID NO:1 is identical to the characteristic sequence conserved highly in the Gs and Golf proteins.

The specification also provides guidance and examples of amino acid substitution, deletion or addition in the amino acid sequence of SEQ ID NO:1 causing no loss of the biological functions, such as from page 28, line 21, to page 29, line 20. For example, such amino acid substitution, deletion or addition in the amino acid sequence of SEQ ID NO:1 can be introduced into a portion having low homology with the amino acid sequences of various G protein α subunits which have already been identified. Also for example, in the case of an amino acid substitution, an amino acid can be substituted by another amino acid having the characteristics similar to those of the original amino acid in terms of polarity, electric charge, solubility, hydrophilicity/hydrophobicity, polarity and the like, in view of the maintenance of the protein structure.

Moreover, the specification has provided a reasonable number and sufficiently representative sequences falling within the scope of the claimed genus, nucleotide sequences encoding the amino acid sequence of SEQ ID NOs: 25 and 26, as described from page 29, line 21, to page 30, line 8. A polynucleotide comprising the nucleotide sequence of SEQ ID NO:2 has been obtained from a human brain-derived cDNA library, and encodes the amino acid sequence of SEQ ID NO:1, as described in Example 1. A polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 has been obtained from a mouse brain-derived cDNA library, and encodes the amino acid sequence of SEQ ID NO:25, as described in Example 26. A polynucleotide comprising the nucleotide sequence of SEQ ID NO:28 has been obtained from a rat brain-derived cDNA library, and encodes the amino acid sequence of SEQ ID NO:26, as described in Example 27.

Comparisons of the sequence listings of SEQ ID NO:1 and any of SEQ ID NOs:25 and 26 are provided at the website of the Public PAIR provided by the U.S. Patent and Trademark Office of the present application, under the tab "Supplemental Content" and Item ID 333667. Enclosed is a copy of a printout of the Supplemental Content page, pages 1 and 2 identifying the searches done and pages 5 to 8 showing the comparisons. Based on the comparisons, it is clear

that: (A) SEQ ID NO:25 has a matching score of 88.5% with SEQ ID NO:1 and retains amino acid sequences represented by amino acid Nos. 119 to 133, 287 to 292, 353 to 359, and 428 to 435 of SEQ ID NO:1, as shown in Result 3; and (B) SEQ ID NO:26 has a matching score of 88.0% with SEQ ID NO:1 and retains amino acid sequences represented by amino acid Nos. 119 to 133, 287 to 292, 353 to 359, and 428 to 435 of SEQ ID NO:1, as shown in Result 4.

Thus, the subject matter recited in amended claim 7 is well described in the specification and the specification provides sufficient guidance to enable one of the ordinary skill in the art to make and use the claimed invention. Accordingly, reconsideration and withdrawal of the rejections under 35 U.S.C. § 112, first paragraph, are respectfully requested.

Claim Rejections – 35 U.S.C. § 102

The search result shown in Section 10 of the Office Action appear to have been obtained using as a query the amino acid sequence represented by amino acid numbers 96 to 126 of SEQ ID NO:1 of the present invention, and is relied upon to support the conclusion that Drmanac teaches the amino acid sequence of SEQ ID NO:31595 which assertedly has a best local similarity score of 100% to the amino acid sequence represented by amino acid numbers 96 to 126 of SEQ ID NO:1 of the present invention.

Attached is an alignment of SEQ ID NO:1 of the present invention and SEQ ID NO:31595 of Drmanac over their entire length generated using the maximum matching program of the gene analysis software GENETYX™ version 8.0.1 (GENETYX Corporation) with default parameters. According to the attached alignment, the portion of the amino acid sequence represented by amino acid numbers 1 to 126 of SEQ ID NO:31595 of Drmanac *et al.* is identical to the sequence represented by amino acid numbers 1 to 126 of SEQ ID NO:1 of the present invention, but the larger portion of the amino acid sequence represented by amino acid numbers 127 to 461 of SEQ ID NO:31595 of Drmanac differs greatly from the sequence represented by amino acid numbers 127 to 458 of SEQ ID NO:1 of the present invention. The matching score of SEQ ID NO:1 of the present invention and SEQ ID NO:31595 of Drmanac over their entire length is only 36.94%. Moreover, SEQ ID NO:31595 of Drmanac does not contain amino acid sequences identical to amino acid sequences represented by the amino acid numbers 119 to 133, 287 to 292, 353 to 359 and 428 to 435 of SEQ ID NO:1 of the present invention.

Therefore, the polynucleotide recited in amended claim 7 is not anticipated by Drmanac. Nor is the polynucleotide of amended claim 7 rendered obvious by Drmanac. Similarly,

dependent claims 13-17 and 23 and 24 are neither anticipated by nor rendered obvious over Drmanac.

Reconsideration and withdrawal of the rejections, and rejoinder of at least the claims of provisionally elected Group II are respectfully requested. An early Notice of Allowance of these and all other rejoinable claims, such as claims 33-39, is also respectfully solicited.

Respectfully submitted,

YASUHIKO TAKAHASHI *et al.*

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(Date)

ALAN S. NADEL
Registration No. 27,363
AKIN GUMP STRAUSS HAUER & FELD LLP
One Commerce Square
2005 Market Street, Suite 2200
Philadelphia, PA 19103-7013
Telephone: 215-965-1200
Direct Dial: 215-965-1280
Facsimile: 215-965-1210
E-Mail: anadel@akingump.com

ASN:hg